

OIPF

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,403

DATE: 12/21/2001

TIME: 12:08:06

Input Set : A:\farrell.psu.us.txt

Output Set: N:\CRF3\12212001\J006403.raw

**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Farrell, David  
4 Al-Mondhiry, Hamid  
6 <120> TITLE OF INVENTION: A MONOCLONAL ANTIBODY-BASED DIAGNOSTIC ASSAY FOR GAMMA  
FIBRINOGEN  
8 <130> FILE REFERENCE: P05375US1  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/006,403  
C--> 10 <141> CURRENT FILING DATE: 2001-12-05  
10 <160> NUMBER OF SEQ ID NOS: 1  
12 <170> SOFTWARE: PatentIn version 3.0  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 20  
16 <212> TYPE: PRT  
17 <213> ORGANISM: Synthetic construct -invalid, see error summary sheet item 10  
19 <400> SEQUENCE: 1  
21 Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr Pro  
22 1 5 10 15  
24 Glu Asp Asp Leu  
25 20

VERIFICATION SUMMARY

DATE: 12/21/2001

PATENT APPLICATION: US/10/006,403

TIME: 12:08:07

Input Set : A:\farrell.psu.us.txt

Output Set: N:\CRF3\12212001\J006403.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 101006403

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics  
Wrapped Aminos**    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ **Invalid Line Length**    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☐ **Misaligned Amino  
Numbering**    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4 ☐ **Non-ASCII**    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ **Variable Length**    Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ **PatentIn 2.0  
"bug"**    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7 ☐ **Skipped Sequences  
(OLD RULES)**    Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ **Skipped Sequences  
(NEW RULES)**    Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
  
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)**    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☒ **Invalid <213>  
Response**    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ **Use of <220>**    Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ **PatentIn 2.0  
"bug"**    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.